

## SEQUENCE LISTING

<110> Whitsett, Jeffrey  
Klaus H. Kaestner

<120> Diagnosis, prognosis and treatment of  
pulmonary diseases

<130> 10872/517745

<150> 60/519,453  
<151> 2004-11-12

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aaaagaggggt ggggggtgggg ggtgattgtc ggtcgttgt tgtagctttt aaattttaaa 180  
ctgccatca ctcggcttcc agt atg ctg gga gcg gtg aag atg gaa ggg cac 233

Met Leu Gly Ala Val Lys Met Glu Gly His

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15 20 25

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Ser Val Ser Asn Met Asn Ala Gly Leu Gly Met Asn Gly Met Asn Thr

30 35 40

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Tyr Met Ser Met Ser Ala Ala Met Gly Ser Gly Ser Gly Asn Met

45 50 55

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Ser Ala Gly Ser Met Asn Met Ser Ser Tyr Val Gly Ala Gly Met Ser

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75            80            85            90

ggc ggc tcg gcc ggg ggc ggc gtg gcg ggc atg ggg ccg cac ttg 521  
Gly Gly Ser Ala Gly Ala Ala Gly Val Ala Gly Met Gly Pro His Leu  
95            100            105

agt ccc agc ctg agc ccc ctc ggg ggg cag gcg gcc ggg gcc atg ggc 569  
Ser Pro Ser Leu Ser Pro Leu Gly Gly Gln Ala Ala Gly Ala Met Gly  
110            115            120

ggc ctg gcc ccc tac gcc aac atg aac tcc atg agc ccc atg tac ggg 617  
Gly Leu Ala Pro Tyr Ala Asn Met Asn Ser Met Ser Pro Met Tyr Gly  
125            130            135

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Gln Ala Gly Leu Ser Arg Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser  
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Tyr Thr His Ala Lys Pro Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met  
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gcc atc cag cag agc ccc aac aag atg ctg acg ctg agc gag atc tac 761  
Ala Ile Gln Gln Ser Pro Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr  
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Gln Trp Ile Met Asp Leu Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg  
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tgg cag aac tcc atc cgc cac tcg ctc tcc aac gac tgt ttc ctg 857  
Trp Gln Asn Ser Ile Arg His Ser Leu Ser Phe Asn Asp Cys Phe Leu  
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ctg cac cct gac tcg ggc aac atg ttc gag aac ggc tgc tac ctg cgc 953  
Leu His Pro Asp Ser Gly Asn Met Phe Glu Asn Gly Cys Tyr Leu Arg  
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 Ala Gly Thr Glu Ser Pro His Ser Ser Ala Ser Pro Cys Gln Glu His  
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agc ccc cca gag ccg gcg ccc tct ccc ggg cag cag cag cag cag gcc gcg 1241  
Ser Pro Pro Glu Pro Ala Pro Ser Pro Gly Gln Gln Gln Gln Ala Ala  
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gcc cac ctg ctg ggc ccg ccc cac cac ccg ggc ctg ccg cct gag gcc 1289  
Ala His Leu Leu Gly Pro Pro His His Pro Gly Leu Pro Pro Glu Ala  
350 355 360

cac ctg aag ccg gaa cac cac tac gcc ttc aac cac ccg ttc tcc atc 1337  
His Leu Lys Pro Glu His His Tyr Ala Phe Asn His Pro Phe Ser Ile  
365 370 375

aac aac ctc atg tcc tcg gag cag cag cac cac cac agc cac cac cac 1385  
Asn Asn Leu Met Ser Ser Glu Gln Gln His His His Ser His His His  
380 385 390

cac caa ccc cac aaa atg gac ctc aag gcc tac gaa cag gtg atg cac 1433  
His Gln Pro His Lys Met Asp Leu Lys Ala Tyr Glu Gln Val Met His  
395 400 405 410

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Tyr Pro Gly Tyr Gly Ser Pro Met Pro Gly Ser Leu Ala Met Gly Pro  
415 420 425

gtc acg aac aaa acg ggc ctg gac gcc tcg ccc ctg gcc gca gat acc 1529  
Val Thr Asn Lys Thr Gly Leu Asp Ala Ser Pro Leu Ala Ala Asp Thr  
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Ser Tyr Tyr Gln Gly Val Tyr Ser Arg Pro Ile Met Asn Ser Ser \*  
145 150 155

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cataacaccc ccaccccaac acccccaaga cagcagtctt ctccacccgc tgcatggcgtt 1757  
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gtttaaacag aaccagaggg ttgtactatt gttaaaaaac agaaaaaaaataatgtaa 2057  
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65              70              75              80  
Ser Pro Gly Ala Gly Ala Met Ala Gly Met Gly Gly Ser Ala Gly Ala  
85              90              95  
Ala Gly Val Ala Gly Met Gly Pro His Leu Ser Pro Ser Leu Ser Pro  
100            105            110  
Leu Gly Gly Gln Ala Ala Gly Ala Met Gly Gly Leu Ala Pro Tyr Ala  
115            120            125  
Asn Met Asn Ser Met Ser Pro Met Tyr Gly Gln Ala Gly Leu Ser Arg  
130            135            140  
Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser Tyr Thr His Ala Lys Pro  
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Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met Ala Ile Gln Gln Ser Pro  
165            170            175  
Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr Gln Trp Ile Met Asp Leu  
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Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg Trp Gln Asn Ser Ile Arg  
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Gly Lys Lys Ala Ala Ala Gly Ala Gln Ala Ser Gln Ala Gln Leu Gly		
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Glu Ala Ala Gly Pro Ala Ser Glu Thr Pro Ala Gly Thr Glu Ser Pro		
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His Ser Ser Ala Ser Pro Cys Gln Glu His Lys Arg Gly Gly Leu Gly		
305	310	315
Glu Leu Lys Gly Thr Pro Ala Ala Ala Leu Ser Pro Pro Glu Pro Ala		
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Pro Ser Pro Gly Gln Gln Gln Ala Ala Ala His Leu Leu Gly Pro		
340	345	350
Pro His His Pro Gly Leu Pro Pro Glu Ala His Leu Lys Pro Glu His		
355	360	365
His Tyr Ala Phe Asn His Pro Phe Ser Ile Asn Asn Leu Met Ser Ser		
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Glu Gln Gln His His His Ser His His His Gln Pro His Lys Met		
385	390	395
Asp Leu Lys Ala Tyr Glu Gln Val Met His Tyr Pro Gly Tyr Gly Ser		
405	410	415
Pro Met Pro Gly Ser Leu Ala Met Gly Pro Val Thr Asn Lys Thr Gly		
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 cccgaggccg ttccgggtct gaactgtaac agggaggggc ctgcaggag cagcagcggg 180  
 cgagttaaag t atg ctg gga gcg gtg aag atg gaa ggg cac gag ccg tcc 230  
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 Asp Trp Ser Ser Tyr Tyr Ala Glu Pro Glu Gly Tyr Ser Ser Val Ser  
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aac atg aac gcc ggc ctg ggg atg aac ggc atg aac acg tac atg agc 326  
 Asn Met Asn Ala Gly Leu Gly Met Asn Gly Met Asn Thr Tyr Met Ser  
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atg tcg gcg gcc ggc atg ggc agc ggc tcg ggc aac atg agc gcg ggc 374  
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gcc ggg gcg gcc ggc gtg gcg ggc atg ggg ccg cac ttg agt ccc agc 518  
Ala Gly Ala Ala Gly Val Ala Gly Met Gly Pro His Leu Ser Pro Ser  
95 100 105

ctg agc ccg ctc ggg ggg cag gcg gcc ggg ggc atg ggc ggc ctg gcc 566  
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110 115 120 125

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Pro Tyr Ala Asn Met Asn Ser Met Ser Pro Met Tyr Gly Gln Ala Gly  
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ctg agc cgc gcc cgc gac ccc aag acc tac agg cgc agc tac acg cac 662  
Leu Ser Arg Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser Tyr Thr His  
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Ala Lys Pro Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met Ala Ile Gln  
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cag agc ccc aac aag atg ctg acg ctg agc gag atc tac cag tgg atc 758  
Gln Ser Pro Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr Gln Trp Ile  
175 180 185

atg gac ctc ttc ccc ttc tac cgg cag aac cag cag cgc tgg cag aac 806  
Met Asp Leu Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg Trp Gln Asn  
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tcc atc cgc cac tcg ctc tcc aac gac tgt ttc ctg aag gtg ccc 854  
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cgc tcg ccc gac aag ccc ggc aag ggc tcc ttc tgg acc ctg cac cct 902  
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225 230 235

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Asp Ser Gly Asn Met Phe Glu Asn Gly Cys Tyr Leu Arg Arg Gln Lys  
240 245 250

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Arg Phe Lys Cys Glu Lys Gln Leu Ala Leu Lys Glu Ala Ala Gly Ala  
255 260 265

gcc ggc agc ggc aag aag ggc gcc gga gcc cag gcc tca cag gct 1046  
Ala Gly Ser Gly Lys Lys Ala Ala Gly Ala Gln Ala Ser Gln Ala  
270 275 280 285

caa ctc ggg gag gcc ggc ggg ccg gcc tcc gag act ccg gcg ggc acc 1094  
Gln Leu Gly Glu Ala Ala Gly Pro Ala Ser Glu Thr Pro Ala Gly Thr

290

295

300

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 305 310 315

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 335 340 345

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 385 390 395

cac aaa atg gac ctc aag gcc tac gaa cag gtg atg cac tac ccc ggc 1430  
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 Tyr Gly Ser Pro Met Pro Gly Ser Leu Ala Met Gly Pro Val Thr Asn  
 415 420 425

aaa acg ggc ctg gac gcc tcg ccc ctg gcc gca gat acc tcc tac tac 1526  
 Lys Thr Gly Leu Asp Ala Ser Pro Leu Ala Ala Asp Thr Ser Tyr Tyr  
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 450 455

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aaaaaaaaatgtcataa aaatataaaa cggtgctgtg actcacctgc tcttagccgc 180  
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cacacgaaat tggacacc tggattttggg ccaactattt ccattttctt ccatttcata 360  
gagagaagag ttgggactg tttccatcata tccttagtac attttcagaa ccaagaaaaga 420  
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cggcttggt agctaacaat ataaatgaca tactctgtt tttcatgtt tgttttttt 540  
ggggagacaa ggttcttc tgcgtttccgg atgtctgaa actcactcta tagacttaggt 600  
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<210> 6  
<211> 1002  
<212> DNA  
<213> homo sapiens

<220>  
<221> promoter  
<222> (1)...(1001)  
<223> upstream promoter for FoxA1 from -1000 to 0

<400> 6  
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<210> 7  
<211> 1001  
<212> DNA  
<213> homo sapiens

<220>  
<221> promoter  
<222> (1)...(1001)  
<223> upstream promoter for FoxA2 from -1000 to 0

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